Application No.:

10/573,372

Filing Date:

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AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0026] on page 8 of the specification as filed with the following:

[0026] In some embodiments, the domain corresponding to residues 1-167 of Figure 2 comprises a sequence according to Formula (I) (SEQ ID NO: 05):

wherein:

each of $\Phi_{1\text{-}10}$ is independently selected from any hydrophobic amino acid residue, Zaa is a neutral/polar amino acid residue, each of $\Sigma aa_{1\text{-}4}$ is independently selected from any small amino acid residue, each of $Baa_{1\text{-}3}$ is independently selected from any basic amino acid residue, each of $Aaa_{1\text{-}5}$ is independently selected from any acidic amino acid residue, each of $Aaa_{1\text{-}2}$ is independently selected from any charged amino acid residue, and $Aaa_{1\text{-}33}$ are each independently selected from any amino acid residue.

Please replace paragraph [0037] on pages 10-11 of the specification as filed with the following:

[0037] In some embodiments, the domain corresponding to residues 168-536 of Figure 2 comprises a sequence according to Formula (II) (SEQ ID NO: 06):

 $Arg-Xaa_1-Xaa_2-Thr-\Sigma aa_1-Ser-\Phi aa_1-Leu-Thr-Glu-\Sigma aa_2-Xaa_3-\Phi aa_2-\Phi aa_3-Gly-Arg-Xaa_4-Gln-\mathring Aaa_1-Baa_1-Glu-Xaa_5-\Phi aa_4-\Phi aa_5-\Omega aa_1-Leu-Leu-Leu-\mathring Aaa_2-\Sigma aa_3-\Sigma aa_4-Xaa_6-Gly-Xaa_7-Xaa_8-\Sigma aa_5-Phe-\Sigma aa_6-Val-\Phi aa_6-Pro-\Phi aa_7-Val-Gly-\Phi aa_8-Gly-Gly-Xaa_9-Gly-Lys-Thr-Thr-Leu-\Sigma aa_7-Gln-Leu-\Phi aa_9-\Phi aa_{10}-Asn-Asp-Xaa_{10}-Arg-Val-Xaa_{11}-Xaa_{12}-Xaa_{13}-Phe-Xaa_{14}-Leu-Baa_2-\Phi aa_{11}-Trp-Val-Cys-Val-Ser-Asp-Xaa_{15}-Phe-Xaa_{16}-Val-Lys-Arg-\Phi aa_{12}-Thr-Baa_3-Glu-Ile-Xaa_{17}-Glu-Xaa_{18}-Ala-Thr-Xaa_{19}-Xaa_{20}-\Omega aa_2-Xaa_{21}-Xaa_{22}-Asp-Xaa_{23}-Xaa_{24}-Asn-Leu-Xaa_{25}-Xaa_{26}-Leu-Gln-Xaa_{27}-Xaa_{28}-Leu-Lys-Glu-\Omega aa_3-Ile-Xaa_{29}-\Sigma aa_8-Xaa_{30}-Xaa_{31}-Phe-Leu-Leu-Val-Leu-Asp-Asp-Val-Trp-$

Application No.:

10/573,372

Filing Date:

October 31, 2006

 $Xaa_{32}\text{-}Glu\text{-}Xaa_{33}\text{-}Xaa_{34}\text{-}Xaa_{35}\text{-}\Omega aa_4\text{-}Trp\text{-}Glu\text{-}Xaa_{36}\text{-}Leu\text{-}Xaa_{37}\text{-}Ala\text{-}Pro\text{-}Leu\text{-}\Omega aa_5\text{-}Xaa_{38}\text{-}\Sigma aa_9\text{-}} \\ \Sigma aa_{10}\text{-}Arg\text{-}Gly\text{-}Ser\text{-}Xaa_{39}\text{-}Val\text{-}Ile\text{-}Val\text{-}Thr\text{-}Thr\text{-}Xaa_{40}\text{-}Xaa_{41}\text{-}Xaa_{42}\text{-}Lys\text{-}\Phi aa_{13}\text{-}Ala\text{-}Xaa_{43}\text{-}\Phi aa_{14}\text{-}} \\ Xaa_{44}\text{-}Gly\text{-}Thr\text{-}Met\text{-}\Omega aa_{6}\text{-}Xaa_{45}\text{-}\Phi aa_{15}\text{-}Xaa_{46}\text{-}Leu\text{-}Å aa_{3}\text{-}Xaa_{47}\text{-}Leu\text{-}Xaa_{48}\text{-}Å aa_{4}\text{-}Asp\text{-}Xaa_{49}\text{-}Xaa_{50}\text{-}} \\ Trp\text{-}Xaa_{51}\text{-}Leu\text{-}\Phi aa_{16}\text{-}\Omega aa_{7}\text{-}Xaa_{52}\text{-}Xaa_{53}\text{-}\Sigma aa_{11}\text{-}Phe\text{-}Xaa_{54}\text{-}Xaa_{55}\text{-}Xaa_{56}\text{-}Xaa_{57}\text{-}Xaa_{58}\text{-}\Sigma aa_{12}\text{-}Xaa_{59}\text{-}} \\ Xaa_{60}\text{-}Xaa_{61}\text{-}Xaa_{62}\text{-}\Omega aa_{8}\text{-}\Phi aa_{17}\text{-}Glu\text{-}Xaa_{63}\text{-}Ile\text{-}Gly\text{-}Arg\text{-}Lys\text{-}Ile\text{-}Ala\text{-}Xaa_{64}\text{-}Lys\text{-}\Phi aa_{18}\text{-}Xaa_{65}\text{-}Gly\text{-}Xaa_{66}\text{-}Pro\text{-}\Phi aa_{19}\text{-}\Sigma aa_{13}\text{-}Ala\text{-}Xaa_{67}\text{-}\Sigma aa_{14}\text{-}\Phi aa_{20}\text{-}Gly\text{-}Xaa_{68}\text{-}\Phi aa_{21}\text{-}Leu\text{-}Arg\text{-}Xaa_{69}\text{-}\Omega aa_{9}\text{-}Xaa_{70}\text{-}\Sigma aa_{15}\text{-}Xaa_{71}\text{-}Xaa_{72}\text{-}Xaa_{73}\text{-}Trp\text{-}Arg\text{-}Xaa_{74}\text{-}\Phi aa_{22}\text{-}\Phi aa_{23}\text{-}Glu\text{-}\Sigma aa_{16}\text{-}Glu\text{-}Xaa_{75}\text{-}Trp\text{-}Xaa_{76}\text{-}\Phi aa_{24}\text{-}Pro\text{-}Xaa_{77}\text{-}Ala\text{-}Xaa_{78}\text{-}Xaa_{79}\text{-}Å aa_{5}\text{-}\Phi aa_{25}\text{-}Leu\text{-}\Sigma aa_{17}\text{-}Xaa_{80}\text{-}Leu\text{-}Xaa_{81}\text{-}Xaa_{82}\text{-}Ser\text{-}Tyr\text{-}Xaa_{83}\text{-}Xaa_{84}\text{-}Leu\text{-}Pro\text{-}\Sigma aa_{18}\text{-}Xaa_{85}\text{-}Leu\text{-}Baa_{4}\text{-}Xaa_{86}\text{-}Cys\text{-}Phe\text{-}Ala\text{-}Phe\text{-}Cys\text{-}Ala\text{-}\Phi aa_{26}\text{-}Phe\text{-}Xaa_{87}\text{-}Lys\text{-}Xaa_{88}\text{-}Vrg\text{-}Xaa_{89}\text{-}Phe\text{-}Xaa_{90}\text{-}Lys\text{-}\Omega aa_{10}\text{-}Xaa_{91}\text{-}Leu\text{-}Ile\text{-}Xaa_{92}\text{-}Xaa_{93}\text{-}Trp\text{-}Ile\text{-}Ala\text{-}Xaa_{94}\text{-}Xaa_{95}\text{-}\Phi aa_{27}\text{-}Ile$

wherein:

each of $\Phi_{1\text{-}27}$ is independently selected from any hydrophobic amino acid residue, each of $\Sigma aa_{1\text{-}18}$ is independently selected from any small amino acid residue, each of $Baa_{1\text{-}4}$ is independently selected from any basic amino acid residue, each of $Aaa_{1\text{-}5}$ is independently selected from any acidic amino acid residue, each of $\Omega aa_{1\text{-}10}$ is independently selected from any charged amino acid residue, and

Xaa₁₋₉₅ are each independently selected from any amino acid residue.

Please replace paragraph [0056] on pages 15-16 of the specification as filed with the following:

[0056] In some embodiments, the domain corresponding to residues 537-1476 of Figure 2 comprises a sequence according to Formula (III) (SEQ ID NO: 07):

 $Leu-Xaa_1-\Omega aa_1-Xaa_2-\Phi aa_1-Phe-Baa_1-Xaa_3-Leu-Xaa_4-Arg-Ile-Baa_2-Val-Leu-Xaa_5-\Phi aa_2-Xaa_6-Xaa_7-Cys-Xaa_8-\Phi aa_3-Baa_3-Xaa_9-Leu-Pro-Xaa_{10}-Xaa_{11}-\Phi aa_4-Gly-Xaa_{12}-Leu-Xaa_{13}-Xaa_{14}-Leu-Arg-Tyr-Leu-Xaa_{15}-\Phi aa_5-Ser-Xaa_{16}-Asn-\Sigma aa_1-Xaa_{17}-Ile-Gln-Arg-Leu-Pro-Glu-Ser-\Phi aa_6-Xaa_{18}-\Omega aa_2-Leu-Xaa_{19}-Xaa_{20}-Leu-Gln-\Sigma aa_2-Leu-Xaa_{21}-Leu-Xaa_{22}-Gly-Cys-Xaa_{23}-Leu-Xaa_{24}-Xaa_{25}-\Phi aa_7-Pro-Xaa_{26}-\Sigma aa_3-Met-Ser-Baa_4-Leu-\Phi aa_8-Xaa_{27}-Leu-Arg-Gln-Leu-Baa_5-Xaa_{28}-Xaa_{29}-Xaa_{30}-Aaa_1-\Phi aa_9-Ile-\Sigma aa_4-\Omega aa_3-Ile-Xaa_{31}-\Omega aa_4-Val-Gly-Baa_6-Leu-Ile-Xaa_{32}-Leu-Gln-Glu-Leu-Xaa_{33}-Ala-\Phi aa_{10}-Xaa_{34}-Val-Xaa_{35}-Xaa_{36}-Baa_7-Xaa_{37}-Gly-Xaa_{38}-Xaa_{39}-\Phi aa_{11}-Ala-Glu-Leu-Ser-Aaa_{10}-Xaa_{10}-Aaa_{10}-Xaa_{10}-Aaa_{$

Application No.:

10/573,372

Filing Date:

October 31, 2006

$$\begin{split} & \Sigma aa_{5} - \Phi aa_{12} - Xaa_{40} - Gln-Leu-Baa_{8} - \Sigma aa_{6} - Xaa_{41} - Leu-Xaa_{42} - Ile-Xaa_{43} - Asn-Leu-Xaa_{44} - Asn-Val-Xaa_{45} - Xaa_{46} - Xaa_{47} - \Omega aa_{5} - Glu-\Sigma aa_{7} - Xaa_{48} - Lys-Ala-Baa_{9} - Leu-\Omega aa_{6} - \Omega aa_{7} - Lys-Gln-Xaa_{49} - Leu-\Omega aa_{8} - Xaa_{50} - Leu-Åaa_{2} - Leu-\Omega aa_{9} - Trp-Ala-Xaa_{51} - Gly-Xaa_{52} - Xaa_{53} - Xaa_{54} - Xaa_{55} - Xaa_{56} - Xaa_{57} - Xaa_{58} - Glu-Xaa_{59} - Xaa_{60} - Xaa_{61} - Xaa_{62} - \Omega aa_{10} - \Omega aa_{11} - Val-Leu-Xaa_{63} - Gly-Leu-Xaa_{64} - Pro-His-Xaa_{65} - Xaa_{66} - Leu-Baa_{10} - Xaa_{67} - Leu-\Sigma aa_{8} - Ile-Baa_{11} - Xaa_{68} - Tyr-\Sigma aa_{9} - Gly-\Sigma aa_{10} - \Sigma aa_{11} - Xaa_{69} - Pro-Ser-Trp-\Phi aa_{13} - Xaa_{70} - Xaa_{71} - Xaa_{72} - \Phi aa_{14} - Leu-Pro-Asn-\Phi aa_{15} - Xaa_{73} - Thr-\Phi aa_{16} - Baa_{12} - Leu-\Omega aa_{12} - Xaa_{74} - Cys-\Sigma aa_{12} - Arg-Leu-Xaa_{75} - Xaa_{76} - Leu-\Sigma aa_{13} - Xaa_{77} - \Phi aa_{17} - Gly-Gln-Leu-Xaa_{78} - Xaa_{79} - Leu-Baa_{13} - Xaa_{80} - Leu-His-\Phi aa_{18} - \Omega aa_{13} - Xaa_{81} - Met-\Sigma aa_{14} - Xaa_{82} - Val-Baa_{14} - Gln-\Phi aa_{19} - Xaa_{83} - Xaa_{84} - Xaa_{85} - \Phi aa_{20} - Xaa_{86} - Gly-Xaa_{87} - \Sigma aa_{15} - \Omega aa_{14} - Xaa_{88} - Xaa_{89} - Xaa_{90} - Phe-Pro-Xaa_{91} - Leu-Glu-Xaa_{92} - Leu-Xaa_{93} - \Phi aa_{21} - \Omega aa_{15} - \Omega aa_{16} - Met-Pro-\Sigma aa_{16} - Leu-\Omega aa_{17} - Glu-\Phi aa_{22} \end{split}$$

wherein:

each of Φ_{1-22} is independently selected from any hydrophobic amino acid residue, each of Σaa_{1-6} is independently selected from any small amino acid residue, each of Baa_{1-14} is independently selected from any basic amino acid residue, each of Aaa_{1-2} is independently selected from any acidic amino acid residue, each of Ωaa_{1-16} is independently selected from any charged amino acid residue, and

Xaa₁₋₉₃ are each independently selected from any amino acid residue.